

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=20; hr=15; min=6; sec=9; ms=551;]

=====

Application No: 10547447 Version No: 2.0

Input Set:**Output Set:**

Started: 2008-02-29 16:55:52.428
Finished: 2008-02-29 16:55:58.398
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 970 ms
Total Warnings: 41
Total Errors: 35
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)

Input Set:

Output Set:

Started: 2008-02-29 16:55:52.428
Finished: 2008-02-29 16:55:58.398
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 970 ms
Total Warnings: 41
Total Errors: 35
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (31)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2008-02-29 16:55:52.428
Finished: 2008-02-29 16:55:58.398
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 970 ms
Total Warnings: 41
Total Errors: 35
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (44) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
Heinz, Ernst
Abbadì, Amine
Domergue, Frederic
Zank, Thorsten

<120> METHOD FOR THE PRODUCTION OF POLYUNSATURATED FATTY ACIDS

<130> 12810-00119-US

<140> 10547447

<141> 2005-08-26

<150> PCT/EP2004/000771

<151> 2001-01-29

<150> DE 103 08 836.9

<151> 2003-02-27

<160> 59

<170> PatentIn version 3.5

<210> 1

<211> 849

<212> DNA

<213> Caenorhabditis elegans

<220>

<221> CDS

<222> (1)..(849)

<223> Acyl-CoA:lysophospholipid acyltransferase

<400> 1

atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc 48

Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu

1 5 10 15

ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att 96

Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile

20 25 30

tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144

Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val

35 40 45

aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt 192

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe

50 55 60

cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val

65 70 75 80

tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt	288
Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys	
85 90 95	
aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg	336
Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro	
100 105 110	
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc	384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe	
115 120 125	
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat	432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr	
130 135 140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg	480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met	
145 150 155 160	
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat	528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn	
165 170 175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca	576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala	
180 185 190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg	624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg	
195 200 205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt	672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val	
210 215 220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat	720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp	
225 230 235 240	
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc	768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala	
245 250 255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt	816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg	
260 265 270	
gga gaa aca aaa gac ggg aag aaa tct gag taa	849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu	
275 280	

<210> 2
 <211> 282
 <212> PRT

<213> Caenorhabditis elegans

<400> 2

Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1 5 10 15

Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
20 25 30

Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
85 90 95

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
100 105 110

Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
115 120 125

Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
130 135 140

Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145 150 155 160

Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
165 170 175

Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
180 185 190

Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
195 200 205

Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
 210 215 220

Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
 225 230 235 240

Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
 245 250 255

Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
 260 265 270

Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
 275 280

<210> 3
 <211> 849
 <212> DNA
 <213> *Caenorhabditis elegans*

<220>
 <221> CDS
 <222> (1)..(849)
 <223> Acyl-CoA:lysophospholipid acyltransferase

<400> 3
 atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc 48
 Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
 1 5 10 15
 ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att 96
 Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
 20 25 30
 tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt 144
 Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
 35 40 45
 aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt 192
 Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
 50 55 60
 cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc 240
 His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
 65 70 75 80
 tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt 288
 Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
 85 90 95
 aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg 336

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro	
100 105 110	
aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc	384
Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe	
115 120 125	
ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat	432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr	
130 135 140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg	480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met	
145 150 155 160	
aag aac aga aat ctt aaa ctt tgg gta tct ccg gaa gga aca aga aat	528
Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn	
165 170 175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca	576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala	
180 185 190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg	624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg	
195 200 205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt	672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val	
210 215 220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat	720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp	
225 230 235 240	
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc	768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala	
245 250 255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt	816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg	
260 265 270	
gga gaa aca aaa gac ggg aag aaa tct gag taa	849
Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu	
275 280	

<210> 4
 <211> 282
 <212> PRT
 <213> Caenorhabditis elegans

<400> 4

Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
1 5 10 15

Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
20 25 30

Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
35 40 45

Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
50 55 60

His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
65 70 75 80

Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
85 90 95

Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
100 105 110

Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
115 120 125

Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
130 135 140

Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
145 150 155 160

Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn
165 170 175

Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
180 185 190

Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
195 200 205

Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
210 215 220

Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
225 230 235 240

<400>	5															
atg	gag	aac	ttc	tgg	tcg	atc	gtc	gtg	ttt	ttt	cta	ctc	tca	att	ctc	48
Met	Glu	Asn	Phe	Trp	Ser	Ile	Val	Val	Phe	Phe	Leu	Leu	Ser	Ile	Leu	
1			5			10			15							
ttc	att	tta	tat	aac	ata	tcg	aca	gta	tgc	cac	tac	tat	gtg	cgg	att	96
Phe	Ile	Leu	Tyr	Asn	Ile	Ser	Thr	Val	Cys	His	Tyr	Tyr	Val	Arg	Ile	
20				25				30								
tcg	ttt	tat	tac	ttc	aca	att	tta	ttg	cat	gga	atg	gaa	gtt	tgt	gtt	144
Ser	Phe	Tyr	Tyr	Phe	Thr	Ile	Leu	Leu	His	Gly	Met	Glu	Val	Cys	Val	
35			40				45									
aca	atg	atc	cct	tct	tgg	cta	aat	ggg	aag	ggc	gct	gat	tac	gtg	ttt	192
Thr	Met	Ile	Pro	Ser	Trp	Leu	Asn	Gly	Lys	Gly	Ala	Asp	Tyr	Val	Phe	
50			55				60									
cac	tcg	ttt	ttc	tat	tgg	tgt	aaa	tgg	act	ggc	gtt	cat	aca	aca	gtc	240
His	Ser	Phe	Phe	Tyr	Trp	Cys	Lys	Trp	Thr	Gly	Val	His	Thr	Thr	Val	
65		70				75				80						
tat	gga	tat	gaa	aaa	aca	caa	gtt	gaa	ggc	ccg	gct	gta	gtt	att	tgt	288
Tyr	Gly	Tyr	Glu	Lys	Thr	Gln	Val	Glu	Gly	Pro	Ala	Val	Val	Ile	Cys	
85				90				95								
aat	cat	cag	agt	tct	ctc	gac	att	cta	tcg	atg	gca	tca	atc	tgg	ccg	336
Asn	His	Gln	Ser	Ser	Leu	Asp	Ile	Leu	Ser	Met	Ala	Ser	Ile	Trp	Pro	
100			105			110										
aag	aat	tgt	gtt	gta	atg	atg	aaa	cga	att	ctt	gcc	tat	gtt	cca	ttc	384
Lys	Asn	Cys	Val	Val	Met	Met	Lys	Arg	Ile	Leu	Ala	Tyr	Val	Pro	Phe	
115			120			125										

ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat	432
Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr	
130 135 140	
aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg	480
Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met	
145 150 155 160	
aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat	528
Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn	
165 170 175	
cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca	576
Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala	
180 185 190	
gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg	624
Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg	
195 200 205	
gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt	672
Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val	
210 215 220	
gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat	720
Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp	
225 230 235 240	
gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc	768
Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala	
245 250 255	
tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt	816
Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg	
260 265 270	
gga gaa aca aaa gac ggg aag aaa tct gag taa	